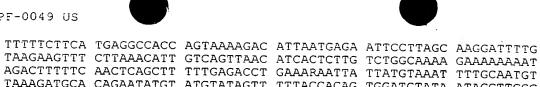
SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Coleman, Roger Stuart, Susan G.
- (ii) TITLE OF THE INVENTION: A NOVEL HUMAN JAK2 KINASE
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/567,508
 - (B) FILING DATE: 05-DEC-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0049US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Placenta
 - (B) CLONE: 179527



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCACGCGTCC GGTTGCCAAC CCGCAGGCGA CTGGGCGCTT CATCCCACCC TCACCCCTTT CCAGCCAAGG TGGCTGATCG GAGTCAGGCT CTCGAGGTCG CATTGCCACG AAACGGNGTG 120 TGTGAGCGCG TTGTCCCCGG NCCCCGGGGC CACTTCCCCT CGGCCTAGNA GACTGGACTG GGGAAGGACG GGTCTGTTGT ACCCGGGAGG TGGAAGGAAAA AGCCGAAAGC GGAGAAGTGT 240 GCGGGAGGGG AGTCTCCGCG CGGAGGNAGA CCGGNCTCCT CCAGTGCAGG TTGTGCGCTG 300 GGGAGCCAGC CASGGCAAAT GTTCTGAAAA AGACTCTGCA TGGGAATGGC CTGCCTTACG ATGACAGAAA TGGAGGGAAC ATCCACCTCT TCTATATATC AGAATGGTGA TATTTCTGGA AATGCCAATT CTATGAAGCA AATAGATCCA GTTCTTCAGG TGTATCTTTA CCATTCCCTT 480 GGGAAATCTG AGGCAGATTA TCTGACCTTT CCATCTGGGG AGTATGTTGG AGAAGAAATC TGTATTGCTG CTTCTAAAGC TTGTGGTATC ACACCTGTGT ATCATAATAT GTTTGCTTTA ATGAGTGAAA CAGAAAGGAT CTGGTATCCA CCCAACCATG TCTTCCATAT AGATGAGTCA 660 ACCAGGCATA ATGTACTCTA CAGAATAAGA TTTTACTTTC CTCGTTGGTA TTGCAGTGGC 720 AGCAACAGAG CCTATCGGCA TGGAATATCT CGAGGTGCTG AAGCTCCTCT TCTTGATGAC TTTGTCATGT CTTACCTCTT TGCTCAGTGG CGGCATGATT TTGTGCATGG ATGGATAAAA GTACCTGTGA CTCATGAAAC ACAGGAAGAA TGTCTTGGGA TGACAGTGTT AGATATGATG AGAATAGCCA AAGAAAACGA TCAAACCCCA CTGGCCATCT ATAACTCTAT CAGCTACAAG ACATTCTTAC CACAATGTAT TCGAGCAAAG ATCCAAGACT ATCATATTTT GACAAGGAAG 1020 CGAATAAGGT ACAGATTTCG CAGATTTATT CAGCAATTCA GCCAATGCAA AGCCACTGCC AGAAACTTGA AACTTAAGTA TCTTATAAAT CTGGAAACTC TGCAGTCTGC CTTCTACACA 1140 GAGAAATTTG AAGTAAAAGA ACCTGGAAGT GGTCCTTCAG GTGAGGAGAT TTTTGCAACC ATTATAATAA CTGGAAACG TGGAATTCAG TGGTCAAGAG GGAAACATAA AGAAAGTGAG ACACTGACAG AACAGGATTT ACAGTTATAT TGCGATTTC CTAATATTAT TGATGTCAGT ATTAAGCAAG CAAACCAAGA GGGTTCAAAT GAAAGCCGAG TTGTAACTAT CCATAAGCAA GATGGTAAAA ATCTGGAAAT TGAACTTAGC TCATTAAGGG AAGCTTTGTC TTTCGTGTCA TTAATTGATG GATATTATAG ATTAACTGCA GATGCACATC ATTACCTCTG TAAAGAAGAGTA 1200 1260 1380 1500 GCACCTCCAG CCGTGCTTGA AAATATACAA AGCAACTGTC ATGGCCCAAT TTCGATGGAT 1560 TTTGCCATTA GTAAACTGAA GAAAGCAGGT AATCAGACTG GACTGTATGT ACTTCGATGC 1620 AGTCCTAAGG ACTTTAATAA ATATTTTTTG ACTTTTGCTG TCGAGCGAGA AAATGTCATT GAATATAAAC ACTGTTTGAT TACAAAAAAT GAGAATGAAG AGTACAACCT CAGTGGGACA
AAGAAGAACT TCAGCAGTCT TAAAGATCTT TTGAATTGTT ACCAGATGA AACTGTTCGC
TCAGACAATA TAATTTTCCA GTTTACTAAA TGCTGTCCCC CAAAGCCAAA AGATAAATCA 1800 AACCTTCTAG TCTTCAGAAC GAATGGTGTT TCTGATGTAC CAACCTCACC AACATTACAG 1920 AGGCCTACTC ATATGAACCA AATGGTGTTT CACAAAATCA GAAATGAAGA TTTGATATTT AATGAAAGCC TTGGCCAAGG CACTTTTACA AAGATTTTTA AAGGCGTACG AAGAGAAGTA 2040 GGAGACTACG GTCAACTGCA TGAAACAGAA GTTCTTTTAA AAGTTCTGGA TAAAGCACAC 2100 AGGAACTATT CAGAGTCTTT CTTTGAAGCA GCAAGTATGA TGAGCAAGCT TTCTCACAAG 2160 CATTIGGITI TAAATTAIGG AGTAIGTGIC TGTGGAGACG AGAATAITCI GGTTCAGGAG TITGIAAAAI TITGAICACT AGAIACAIAI CIGAAAAAGA ATAAAAAITG TAIAAATAIA TIAIGGAAAC TIGAAGTIGC TAAACAGTIG GCAIGGGCCA TGCAITITCI AGAAGAAAAC 2280 2340 ACCCTTATTC ATGGGAATGT ATGTGCCAAA AATATTCTGC TTATCAGAGA AGAAGACAGG AAGACAGGAA ATCCTCCTTT CATCAAACTT AGTGATCCTG GCATTAGTAT TACAGTTTTG 2460 CCAAAGGACA TTCTTCAGGA GAGAATACCA TGGGTACCAC CTGAATGCAT TGAAAATCCT 2520 AAAAATTTAA ATTTGGCAAC AGACAAATGG AGTTTTGGTA CCACTTTGTG GGAAATCTGC 2580 AGTGGAGGAG ATAAACCTCT AAGTGCTCTG GATTCTCAAA GAAAGCTACA ATTTTATGAA GATAGGCATC AGCTTCCTGC ACCAAAGTGG GCAGAATTAG CAAACCTTAT AAATAATTGT 2700 ATGGATTATG AACCAGATTT CAGGCCTTCT TTCAGAGCCA TCATACGAGA TCTTAACAGT TTGTTTACTC CAGATTATGA ACTATTAACA GAAAATGACA TGTTACCAAA TATGAGGATA 2820 GGTGCCTTGG GGTTTTCTGG TGCCTTTGAA GACCGGGATC CTACACAGTT TGAAGAGAGA 2880 CATTTGAAAT TTCTACAGCA ACTTGGCAAG GGTAATTTTG GGAGTGTGGA GATGTGCCGG 2940 TATGACCCTC TACAGGACAA CACTGGGGAG GTGGTCGCTG TAAAAAAGCT TCAGCATAGT 3000 ACTGAAGAGC ACCTAAGAGA CTTTGAAAGG GAAATTGAAA TCCTGAAATC CCTACAGCAT 3060 GACAACATTG TAAAGTACAA GGGAGTGTGC TACAGTGCTG GTCGGCGTAA TCTAAAATTA ATTATGGAAT ATTTACCATA TGGAAGTTTA CGAGACTATC TTCAAAAACA TAAAGAACGG 3180 ATAGATCACA TAAAACTTCT GCAGTACACA TCTCAGATAT GCAAGGGTAT GGAGTATCTT GGTACAAAAA GGTATATCCA CAGGGATCTG GCAACGAGAA ATATATTGGT GGAGAACGAG 3240 3300 AACAGAGTTA AAATTGGRGA TTTTGGGTTA ACCAAAGTCT TGCCACAAGA CAAAGAATAC TATAAAGTAA AAGAACCTGG TGAAAGTCCC ATATTCTGGT ATGCTCCAGA ATCACTGACA 3420 GAGAGCAAGT TTTCTGTGGC CTCAGATGTT TGGAGCTTTG GAGTGGTTCT GTATGAACTT 3480 TTCACATACA TTGAGAAGAG TAAAAGTCCA CCAGCGGAAT TTATGCGTAT GATTGGCAAT GACAAACAAG GACAGATGAT CGTGTTCCAT TTGATAGAAC TTTTGAAGAA TAATGGAAGA TTACCAAGAC CAGATGGATG CCCAGATGAG ATCTATATGA TCATGACAGA ATGCTGGAAC AATAATGTAA ATCAACGCCC CTCCTTTAGG GATCTAGCTC TTCGAGTGGA TCAAATAAGG GATAACATGG CTGGATGAAA GAAATGACCT TCATTCTGAG ACCAAAGTAG ATTTACAGAA CAAAGTTTTA TATTTCACAT TGCTGTGGAC TATTATTACA TATATCATTA TTATATAAAT CATGATGCTA GCCAGCAAAG ATGTGAAAAT ATCTGCTCAA AACTTTCAAA GTTTAGTAAG 3900



						2200
TAAGAAGTTT	CTTAAACATT	GTCAGTTAAC	ATCACTCTTG	TCTGGCAAAA	GAAAAAAAAT	4020
AGACTTTTTC	AACTCAGCTT	TTTGAGACCT	GAAARAATTA	TTATGTAAAT	TTTGCAATGT	4080
TAAAGATGCA	CAGAATATGT	ATGTATAGTT	TTTACCACAG	TGGATGTATA	ATACCTTGGC	4140
ATCTTGTGTG	ATGTTTAACA	CACATGAGGG	CTGGTGTTCA	TTAATACTGT	ΤΤΤΟΟΙΙΟΟΟ	4200
TTCCATGGTT	AATCTATAAT	TAATTACTTC	ACTAAACAAA	CAAATTAAGA	TCTTCTAATT	4260
ATTGAATAAG	TACCTTTGTG	TCCTTGTTCA	TTTATATCCC	TCCCCACCAT	TATAACCACC	
TOTATACTT	TACCTTCTAC	TTCCTTCTTCA	TITALATOOC	TGGCCAGCAI	TATAAGCAGG	4320
TOTATACTT	TAGCTIGIAG	TTCCATGTAC	TGTAAATATT	TTTCACATAA	AGGGAACAAA	4380
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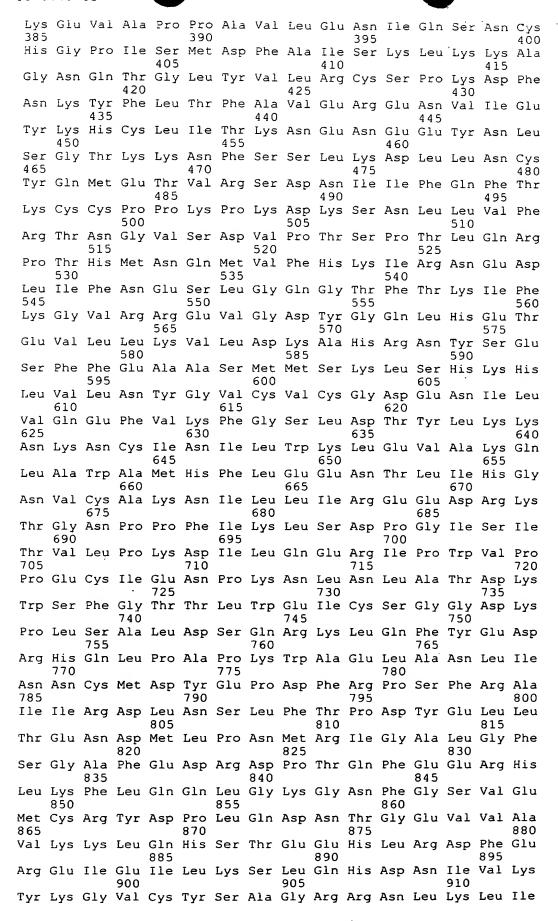
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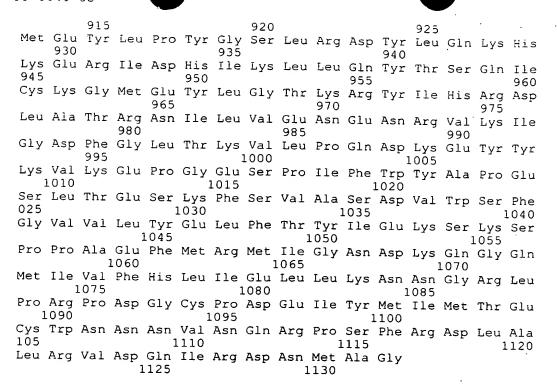
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1132 amino acids

 - (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:

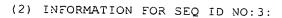
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Gly	Met	Ala	Cys 5	Leu	Thr	Met	Thr	Glu 10	Met	Glu	Gly	Thr	Ser	Thr
			20					25	Ser				30	Ser	Met
		35					40					45			Gly
	50					55					60				Gly
65					Ala 70					75					80
				85	Ala				90					95	-
			100		Phe			105					110		
		115			Phe		120					125			
	130				His	135					140				
145					Met 150					155					160
				165	Ile				170					175	
			180		Thr			185					190		
		195			Leu		200					205			
	210				Ile	215					220				
225					Arg 230					235					240
				245	Thr				250					255	
			260		Gln			265					270		
		275			Gly		280					285			
iie	290	Thr	GIY	Asn	Gly	G1y 295	Ile	Gln	Trp	Ser	Arg 300	Gly	Lys	His	Lys
Glu 305	Ser	Glu	Thr	Leu	Thr 310	Glu	Gln	Asp	Leu	Gln 315	Leu	Tyr	Cys	Asp	Phe 320
Pro	Asn	Ile	Ile	Asp 325	Val	Ser	Ile	Lys	Gln 330	Ala	Asn	Gln	Glu	Gly 335	Ser
			340		Val			345				-	350		
		355			Ser		360					365	Val		
Ile	Asp 370	Gly	Tyr	Tyr	Arg	Leu 375	Thr	Ala	Asp	Ala	His 380	His	Tyr	Leu	Cys









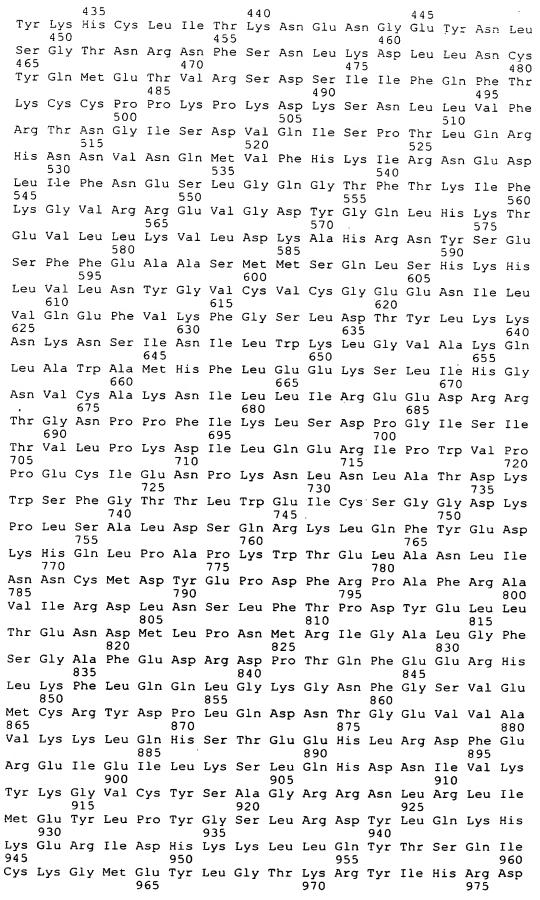
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met 1	Gly	Met	Ala	a Cys	s Lei	ı Thi	r Met	Th	r Glu 10	ı Met	Glu	ı Ala	Thr	Sei 15	Thr
Ser	Pro	Val	His 20	Glr	n Asr	ı Gl	y Asp	25 25	e Pro	Gly	/ Sei	Ala	Asr 30	Ser	. Val
Lys	Gln	Ile 35	Glı	ı Pro	Val	. Le	ı Glr 40		l Tyr	Lei	ı Tyr	His	Ser	Lei	Gly
Gln	Ala 50	Glu	Gly	7 Glu	туг	Leu 55		Phe	Pro	Ser	Gly 60	/ Glu	Tyr	Val	Ala
Glu 65	Glu	Ile	Cys	. Val	. Ala 70	Ala	a Ser	Lys	s Ala	Cys	Gľy	' Ile	Thr	Pro	Val
				85					90	Thr				95	Tyr
			100					105	•				110	Asp	Ile
		115					120	1				125	Ser	Gly	Ser
	130					135	i				140				Leu
145					150					155					Asp 160
				165					170					175	Glu
			180					185					190	_	Glu
		195					200					205	Tyr		
	210					215					220		His		
225					230					235			Gln		240
				245					250				Tyr	255	•
			260					265					Phe 270		
		275					280					285	Ala		
	290					295					300		Lys		
Glu 305					310					315					320
Pro				325					330					335	
Asn			340					345					350		
Glu		355					360					365			
	370					375					380				_
Lys (390					395					400
His				405					410					415	
Gly			420					425					430		
Asn 1	Lys '	Tyr	Phe	Leu	Thr	Phe	Ala	Val	Glu	Arg	Glu	Asn	Val	Ile	Glu







Leu	Ala	Thr	Arg 980	Asn	Ile	Leu	Val	Glu 985	Asn	Glu	Asn	Arg	Val 990	Lys	Ile
Gly	Asp	Phe 995	Gly	Leu	Thr	Lys	Val 1000	Leu	Pro	Gln		Lys	Glu	Tyr	Tyr
	TOTO				Gly	1015					Trp	Tyr			
025					Lys 1030				-	1035				-	1040
			1	1045	Glu			1	Tyr 1050	Ile	Glu	Lys	Ser	Lys	Ser
		ا	1060		Met			Ile 1065	Gly	Asn	Asp	1	Gln	Gly	
		10/5			Leu	. 1	1080				1	Asn 085	Gly	-	
-	1090					1095				1	Val	Ile			
Cys 105	Trp	Asn	Asn	Asn]	Val 1110	Ser	Gln	Arg		Ser 115	Phe	Arg	Asp		Ser 120
Phe	Gly	Trp		Lys .125	Cys	Gly	Thr	Val						•	. 120

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGCGGAAGT GCTCTCGGCG GAAG

24

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGTGTGCTAC AGTGCTGGTC GTCG

24